Swine Outbreak of Pandemic Influenza A Virus on a Canadian Research Farm Supports Human-to-Swine Transmission

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(See the editorial commentary by Gray et al. on pages 19–22).

Background. Swine outbreaks of pandemic influenza A (pH1N1) suggest human introduction of the virus into herds. This study investigates a pH1N1 outbreak occurring on a swine research farm with 37 humans and 1300 swine in Alberta, Canada, from 12 June through 4 July 2009.

Methods. The staff was surveyed about symptoms, vaccinations, and livestock exposures. Clinical findings were recorded, and viral testing and molecular characterization of isolates from humans and swine were performed. Human serological testing and performance of the human influenza-like illness (ILI) case definition were also studied.

Results. Humans were infected before swine. Seven of 37 humans developed ILI, and 2 (including the index case) were positive for pH1N1 by reverse-transcriptase polymerase chain reaction (RT-PCR). Swine were positive for pH1N1 by RT-PCR 6 days after contact with the human index case and developed symptoms within 24 h of their positive viral test results. Molecular characterization of the entire viral genomes from both species showed minor nucleotide heterogeneity, with 1 amino acid change each in the hemagglutinin and nucleoprotein genes. Sixty-seven percent of humans with positive serological test results and 94% of swine with positive swab specimens had few or no symptoms. Compared with serological testing, the human ILI case definition had a specificity of 100% and sensitivity of 33.3%. The only factor associated with seropositivity was working in the swine nursery.

Conclusions. Epidemiologic data support human-to-swine transmission, and molecular characterization confirms that virtually identical viruses infected humans and swine in this outbreak. Both species had mild illness and recovered without sequelae.

Between 2 May 2009 and 5 March 2010, many countries reported pandemic influenza A H1N1 (pH1N1) infection in swine, including the first observation from Canada [1]. Some mentioned human involvement [2, 3], but none presented evidence of human-to-swine transmission other than statements that humans were assumed to be the source or that staff at the swine research farm had respiratory illness or influenza A infection before the animal outbreaks [4, 5]. A Norwegian study established, via temporal relationship and partial genomic sequencing of human and animal viruses, that humans were the source of a swine outbreak [6]. However, this study reported data from 1 farm worker only and otherwise relied on sequence similarities between the swine virus and human isolates from other areas of Norway. We conducted a detailed investigation of a human and swine pH1N1 infection outbreak occurring on a swine research farm in Alberta, Canada, from 12 June through 4 July 2009 with 37 humans and

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1300 swine. We report clinical findings and molecular characterization of the virus in humans and swine, serologic findings, and factors associated with seropositivity in humans.

METHODS

Study Setting

The pH1N1 outbreak occurred from 12 June through 4 July 2009 on a swine research farm in Alberta, Canada. The farm building comprises offices, a lunch room, and a barn that houses 1300 pigs in multiple rooms. Human entry to the barn is restricted and strictly monitored by the farm management. Thirty-seven people (24 of whom were female and 13 of whom were male), including permanent staff, researchers, and students, entered the barn during the outbreak. Strategies to prevent the introduction of disease via humans include the following: changing of clothing and footwear; shower-in, shower-out policies; and prohibiting the entry of person(s) if ill or exposed to other swine in the previous 36 h. New live swine are introduced to the barn from outside sources yearly, the last introduction occurring in September 2008. The ventilation, air quality, and sanitation are superior to Canadian recommendations for commercial swine farms [7], and the barn is secure from the entry of birds. Animal health records are maintained on a daily basis. Sows and gilts are vaccinated during each farrow cycle for classical swine influenza H1N1 (A/swine/Iowa/110600/00) and H3N2 (FluSure; Pfizer Animal Health). This herd is free from the following major swine respiratory pathogens: Porcine Reproductive and Respiratory Syndrome virus (PRRSV), *Mycoplasma hyopneumoniae*, and *Actinobacillus pleuropneumoniae* (APP). This herd is also vaccinated against porcine circovirus type 2 (PCV2) and has shown no symptoms of porcine circoviral disease (PCVD). Before this study, respiratory symptoms were noted in 3 adult swine in December 2008, but nasal swab specimens were negative for influenza A and B viruses by reverse transcriptase polymerase chain reaction (RT-PCR) analysis; symptoms abated within 3 days. No other respiratory symptoms have been recorded in this herd since 2003.

Case Definitions

The clinical definition of human influenza-like illness was acute onset of self-reported fever and cough with one or more of the following: sore throat, arthralgia, myalgia, prostration [8]. A confirmed human case of pH1N1 influenza infection was defined as ILI with a 4-fold increase in antibody titer to pH1N1 and a throat swab specimen positive for pH1N1 by RT-PCR [9]. A probable human case of pH1N1 infection was defined as ILI with at least 1 serum sample having a titer $\geqslant$40 against pH1N1 (and the convalescent pH1N1 titer, if available, the same as or higher than the acute titer) and a throat swab specimen negative for pH1N1 by RT-PCR [10]. A subclinical human case of pH1N1 influenza infection was defined as no ILI, at least 1 serum sample having a titer $\geqslant$40 against pH1N1 (and the convalescent pH1N1 titer, if available, the same as or higher than the acute titer) and a throat swab specimen negative for pH1N1 by RT-PCR. The clinical definition of swine ILI was mild-to-moderate lethargy and anorexia with or without fever or cough. A confirmed case of swine pH1N1 influenza infection was defined as a nasal swab specimen positive for pH1N1 by RT-PCR.

Survey of the Staff at the Swine Farm

Staff were surveyed on 2–3 July 2009 about demographic data, previous influenza vaccination (including swine flu vaccination in 1976), livestock exposures (living on a farm with livestock, number of years working with swine, and areas of work in the barn), and history of any new symptoms in the previous month (cough, fever, runny nose, severe muscle aches, vomiting or diarrhea, or any other symptoms).

Laboratory Investigations

Viral testing. Two humans (the index case and individual 3 in the outbreak investigation) sought medical attention for their ILI and had throat swab specimens collected on 17 June 2009. Subsequent throat swab specimens for the outbreak investigation were collected from 33 of 37 farm workers on 2–4 July 2009 (Table 1). Swab specimens were tested as per manufacturer's instructions for influenza A and B virus; respiratory syncytial virus (RSV); human coronaviruses 229E, OC43, NL63, HKU1; parainfluenza virus; enterovirus or rhinoviruses; and adenoviruses by using the TAG Respiratory Virus Panel (RVP) (Luminex 97 Molecular Diagnostics) nucleic acid amplification assay with suspension microarray detection at the Alberta Provincial Laboratory for Public Health. The pH1N1 subtype was confirmed using primers and probes targeting the hemagglutinin (HA) gene [11]. Samples positive for pH1N1 were sent for complete molecular characterization to the World Health Organization (WHO) Collaborating Center for Studies on the Ecology of Influenza in Animals and Birds, St. Jude Children's Research Hospital (St. Jude), in Memphis, Tennessee.

Nasal swab specimens were initially taken from 38 pigs on 18 June 2009, 1 day before symptoms appeared in swine. Subsequent samples were taken from symptomatic swine and their swine contacts on 25 and 29 June 2009. As symptoms abated, samples taken on 4 July, 14 July, and 11 August 2009 represented 10% of animals from all rooms and populations in the barn. Swab specimens were screened at the Alberta Agriculture and Rural Development Agri-Food Laboratory. Viral RNA was extracted by using the MagMax-96 AI/ND Viral RNA isolation kit (Applied Biosystems), using the protocol for the KingFisher MagMax-96 AI/ND Viral RNA isolation. Extracted RNA was then used as the template in a real-time RT-PCR (RRT-PCR) for detecting the influenza A matrix gene by using the AgPath-ID One-Step RT-PCR Kit (Applied Biosystems/Ambion). The

Table 1. Hemagglutination Inhibition (HI) Titers for Pandemic and Seasonal Influenza Virus, Clinical Findings, Results of Viral Testing, and Case Classifications of Humans Involved in a Pandemic Influenza A Outbreak on a Canadian Swine Farm in 2009

Human tested	HI titers in acute/convalescent serum samples				Clinical signs/symptoms during the outbreak	Throat swab RT-PCR result for influenza	Case definition of human pH1N1 infection
	Pandemic H1N1 A/TN/1/560/09	Seasonal H3N2 A/Brisbane/10/07	Seasonal H1N1 A/Brisbane/59/07	Seasonal B/Florida/4/06			
1	<10/640	<10/20	20/40	<10/<10	ILI	Positive	Confirmed case
2	160/320	<10/<10	40/40	<10/<10	ILI	Negative	Probable case
3	20/160	<10/<10	<10/<10	<10/<10	ILI	Positive	Confirmed case
4	80/320	<10/<10	<10/<10	160/40	ILI	Negative	Probable case
5	<10/no convalescent serum	<10/no convalescent serum	20/no convalescent serum	40/no convalescent serum	ILI	Negative	Incomplete – case status undefined[a]
6	320/640	<10/<10	<10/<10	40/20	ILI	Negative	Probable case
7	No serum sample	No serum sample	No serum sample	No serum sample	ILI	Not done	Incomplete – case status undefined[a]
8	40/no convalescent serum	80/no convalescent serum	80/no convalescent serum	40/no convalescent serum	Fever, headache	Negative	Incomplete– case status undefined[a]
9	<10/160	<10/<10	<10/<10	<10/20	Coryza	Negative	Subclinical case – some symptoms
10	160/160	<10/<10	<10/<10	<10/<10	Sore throat	Negative	Subclinical case – some symptoms
11	160/160	<10/<10	<10/<10	<10/<10	None	Negative	Subclinical case – no symptoms
12	80/640	640/80	<10/40	<10/10	None	Negative	Subclinical case – no symptoms
13	320/1280	320/40	320/160	<10/40	Vomiting	Negative	Subclinical case – some symptoms
14	160/160	160/<10	160/80	160/80	Fever, vomiting	Negative	Subclinical case – some symptoms
15	<10/160	<10/20	<10/10	<10/10	None	Negative	Subclinical case – no symptoms
16	<10/160	<10/<10	<10/<10	160/80	None	Negative	Subclinical case – no symptoms
17	<10/320	<10/20	40/40	<10/40	None	Negative	Subclinical case – no symptoms
18	<10/320	<10/<10	<10/<10	<10/<10	Sore throat, cough, coryza	Negative	Subclinical case – some symptoms
19	<10/no convalescent serum	640/no convalescent serum	<10/no convalescent serum	<10/no convalescent serum	None	Negative	Incomplete – case status undefined[a]
20	<10/<10	<10/<10	<10/<10	<10/<10	None	Negative	Not a case
21	<10/no convalescent serum	640/no convalescent serum	<10/no convalescent serum	<10/no convalescent serum	None	Negative	Incomplete – case status undefined[a]
22	<10/<10	<10/<10	10/20	80/20	None	Negative	Not a case
23	<10/20	<10/20	80/80	<10/<10	None	Negative	Not a case

24	<10/<10	<10/40	<10/<10	<10/10	None	Negative	Not a case
25	<10/20	<10/<10	80/40	<10/<10	None	Negative	Not a case
26	<10/<10	<10/<10	<10/<10	<10/<10	None	Negative	Not a case
27	<10/<10	<10/<10	<10/<10	<10/<10	None	Negative	Not a case
28	<10/<10	<10/<10	<10/<10	<10/<10	None	Negative	Not a case
29	<10/no convalescent serum	<10/no convalescent serum	<10/no convalescent serum	<10/no convalescent serum	None	Negative	Incomplete – case status undefined[a]
30	<10/<10	<10/<10	80/20	<10/<10	None	Negative	Not a case
31	<10/<10	1280/160	<10/<10	<10/<10	Fever, coryza, myalgia, vomit, diarrhea	Negative	Not a case
32	<10/no convalescent serum	<10/no convalescent serum	<10/no convalescent serum	<10/no convalescent serum	Cough, myalgia	Negative	Incomplete - case status undefined[a]
33	No acute serum/20	No acute serum/160	No acute serum/320	No acute serum/40	None	Not done	Incomplete - case status undefined[a]
34	No acute serum/<10	No acute serum/<10	No acute serum/<10	No acute serum/<10	None	Not done	Incomplete - case status undefined[a]
35	No acute serum/<10	No acute serum/10	No acute serum/<10	No acute serum/<10	None	Not done	Incomplete - case status undefined[a]
36	No serum sample	No serum sample	No serum sample	No serum sample	Cough	Negative	Incomplete- case status undefined[a]
37	No serum sample	No serum sample	No serum sample	No serum sample	None	Negative	Incomplete – case status undefined[a]

NOTE. See Materials and Methods for calculation of HI titers and case definitions. ILI, influenza-like illness; RT-PCR, reverse transcriptase polymerase chain reaction.

[a] Serologic data was missing for these individuals, and their data were excluded from analysis.

sequences of the matrix primers, probes, and the RRT-PCR conditions were provided by the National Centre for Foreign Animal Disease, Canadian Food Inspection Agency (NCFAD CFIA). Samples taken on 18 June 2009 were sent to the NCFAD for virus isolation and confirmation of pH1N1. Samples positive for pH1N1 from 29 June 2009 were sent to St. Jude for molecular characterization.

Serological Testing

Serum samples were drawn from staff on 2–4 July 2009 and again on 10–11 August 2009 and sent to St. Jude for analysis. Serum samples were treated with receptor-destroying enzyme and then tested by the hemagglutinin inhibition (HI) assay against A/TN/1/560/2009 (pH1N1) and the seasonal strains A/Brisbane/10/2007 (H3N2), A Brisbane/59/2007 (H1N1), and B/Florida/4/2006, as previously described [12]. An HI titer was defined as the reciprocal of the highest dilution of serum that completely inhibited hemagglutination of a 1% solution of turkey erythrocytes. Serum samples were tested at an initial dilution of 1:10 and a final dilution of 1:1280.

Molecular Characterization

Viral RNA was extracted from virus isolated on Madin Darby canine kidney cells by using RNeasy kits (Qiagen) according to manufacturer's instructions. Reverse transcription and PCR were performed under standard conditions by using WHO-recommended primers specific for each of the 8 gene segments of the pandemic influenza virus [13]. PCR products were purified by using a gel extraction kit (Qiagen). Sequences were compiled and edited by using the Lasergene sequence analysis software package (DNASTAR).

Statistical Analyses

Exploratory analyses of correlates of human seropositivity were done using cross tabulations. Associations were tested using the χ^2 test or the Fisher's exact test at an alpha of .05. Data were analyzed using Stata 9 (University of Texas at Austin, TX).

Ethics

Approval was obtained from the University of Alberta Research Ethics Board (Protocol #00008101), the Conjoint Health Research Ethics Board of the University of Calgary (Ethics ID 18970), McMaster University HHS/FHS Research Ethics Board (REB project # 07-376), and the University of Calgary Animal Care Committee (Protocol M07107).

RESULTS

Human Outbreak

A human outbreak investigation was initiated on 17 June 2009, with notification of the Provincial Medical Officer of Health. The index case (individual 1), a 35-year-old pregnant woman (38 weeks gestation during her ILI) had no prior health conditions. Her last day of contact with swine was 12 June 2009. On the evening of 12 June 2009, she attended a get-together for all of the farm staff. On 13 June 2009, she developed ILI. Individual 2, an otherwise healthy 40-year-old man, developed ILI on 13 June 2009. His last day of contact with swine was 11 June 2009. Individual 3, a 44-year-old otherwise healthy man, and individual 4, an otherwise healthy 25-year-old woman, developed ILI on 16 June 2009. Their last day of contact with swine was 15 June 2009. All 4 individuals had visited all rooms of the barn. Their illness was mild with no requirement for antiviral therapy or hospitalization. Individual 1 did not return to work after this illness and delivered a healthy term infant. Individual 2 returned to work on 15 June but did not have contact with swine; individual 3 returned on 25 June 2009, and individual 4 returned on 22 June 2009. On 18 and 19 June 2009, 3 more persons met the clinical definition of ILI. Their symptoms lasted 5 or 6 days, and they returned to work after a 7-day furlough. They did not require antivirals or hospitalization. No new human clinical ILI cases were documented between 20 June and 12 August 2009. From 17 June 2009, all staff wore N-95 respirators and gloves in the barn, and all staff wore eye protection after 23 June 2009.

Sensitivity and specificity of the human ILI case definition. Of the 25 individuals for whom complete serologic data were available, 15 had positive serological test results and 5 had ILI (Table 1). Compared with serological testing, the ILI definition had a specificity of 100% and a sensitivity of 33.3%, a positive predictive value of 100%, and a negative predictive value of 50%. The presence of any signs or symptoms had a sensitivity 53.3%, a specificity of 90%, a positive predictive value of 88.9%, and a negative predictive value of 56.3%.

Relationship of correlates of seropositivity with survey results. Thirty-two of 37 staff completed the survey. Five (15.6%) lived on a farm with livestock. Four (12.5%) were vaccinated in 2008 for seasonal influenza, and 1 (3.1%) received the swine flu vaccine in 1976. Two weeks before the outbreak, all 32 people had contact with swine in at least 2 different areas of the barn: 12 (37.5%) worked with farrowing swine, 15 (46.9%) worked in the nursery, 22 (68.8%) worked with growers, 16 (50%) worked with sows, and 10 (31.3%) worked with boar studs.

Complete serologic data were available for 25 of the 32 individuals who completed the survey. Working in the swine nursery was the only factor associated with seropositivity for pH1N1. Of the 15 persons working in the nursery, 11 (73.3%) had positive serological test results, compared with 1 of 10 persons not working in the nursery (odds ratio, 18; 95% confidence interval, 1.75–184.7). Age, sex, duration of working with swine, living on a farm with livestock, or prior vaccination against influenza (2008 seasonal or 1976 swine flu) was not associated with seropositivity for pH1N1.

Swine Outbreak

Figure 1 shows the outbreak curve for humans and swine. In swine, the first clinical symptoms were observed on 19 June 2009, 7 days after contact with individuals 1 and 2 and 4 days after contact with individuals 3 and 4. A nonproductive cough with moderate abdominal effort, mild-to-moderate lethargy, pyrexia (temperature, >39.5°C), and anorexia for 24–48 h were observed first in gestating sows. On 19 June 2009, <1% of the entire herd (10 of 1300 swine) showed ILI symptoms; this percentage peaked at 2.5% (33 of 1300 swine) on 21 June 2009. Between 19 June and 4 July 2009, a total of 172 swine (gilts, gestating sows, and lactating sows) showed ILI symptoms. The swine ILI lasted 24–48 h, and all of the animals recovered without antiviral therapy. By 5 July, there were no new swine ILI cases.

On 18 June 2009, a day before symptoms appeared in swine, 12 (32%) of 38 swine tested had nasal swab specimens that were positive for pH1N1 by RT-PCR. On 29 June 2009, 11 days after symptoms started in swine, 16 (59.3%) of 27 swine tested had positive results. On 4 July, 22 (23.2%) of 95 swine tested were positive; on 14 July, 5 (5.5%) of 91 tested were positive; and on 11 August, 1 (.7%) of 145 tested were positive. All swine with positive nasal swab specimens on 18 June, 14 July, and 11 August 2009 were asymptomatic. Of swine with positive nasal swab specimens on 29 June and 4 July 2009, 94% were asymptomatic.

Molecular Characterization of the Virus in Humans and Swine
Full genomic sequencing of viral isolates obtained from individuals 1 (A/Alberta/596/2009) and 3 (A/Alberta/597/2009) on 17 June and 3 swine (A/swine/Alberta/23/2009, A/swine/Alberta/24/2009, and A/swine/Alberta/25/2009) on 29 June revealed minor heterogeneity among isolates at the nucleotide level (Table 2). Nucleotide differences were seen between human and swine pH1N1 isolates at 10 loci in 4 gene segments, and only 2 of these differences (in the HA and nucleoprotein [NP] genes) resulted in amino acid changes. Both at the nucleotide and amino acid levels, these changes were not substantially different between human and swine isolates.

DISCUSSION

Our epidemiologic and clinical findings support human-to-swine transmission of the pH1N1 virus at this swine research farm. No molecular adaptive changes occurred in the virus following transmission from humans to swine, verifying that almost identical viruses infected both species. Most humans and swine had mild or asymptomatic infection, and the ILI case definition showed low sensitivity for pH1N1 infection in humans.

The chronology of events supports human-to-swine transmission: humans became symptomatic and were positive for pH1N1 by RT-PCR before the swine, and the epidemic curve of clinical disease and positive nasal swab specimens in the herd over the next 6 weeks was also consistent with the introduction of an influenza virus by humans. Transmission from humans likely occurred early in their illness, probably before the appearance of any symptoms in individuals with ILI, because pH1N1 viral shedding occurs before the onset of symptoms and peaks on the second day of illness [14]. The chronology of swine infection observed is similar to that seen in an experimental inoculation of swine with pH1N1-like influenza—swine were positive for pH1N1 within 1–4 days, and clinical symptoms developed 4–5 days after exposure [15]. In this outbreak, it is unlikely that the disease originated in swine, because they had no

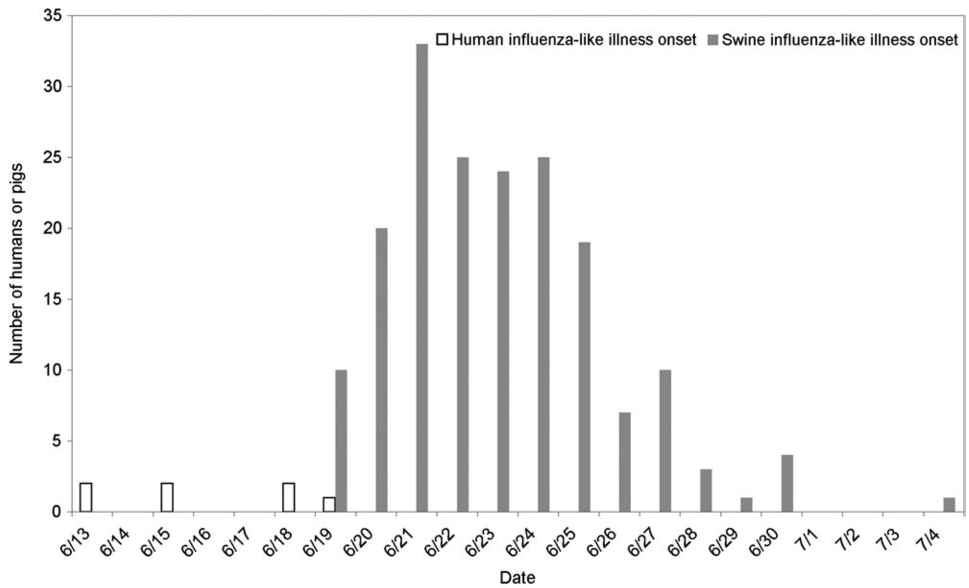

Figure 1. Onset of influenza-like illness among humans and swine during an outbreak of pandemic influenza A on a Canadian swine farm in 2009.

Table 2. Molecular Characterization of Viral Isolates from Humans and Swine during a Pandemic Influenza A Outbreak on a Canadian Swine Farm in 2009

Gene segment	Position[a]	A/swine/Alberta/ 23/2009	A/swine/Alberta/ 24/2009	A/swine/Alberta/ 25/2009	A/Alberta/ 596/2009	A/Alberta/ 597/2009
PA	1290	G	A	G	A	A
	1506	G	G	G	G	A
	1668	A	A	A	A	G
HA	622	A (I)	C (L)	C (L)	C (L)	C (L)
	624	C	C	C	C	A
NP	315	T	T	T	T	C
	1154	A (D)	G (G)	G (G)	G (G)	A (D)
NA	234	A	G	G	G	G
	273	C	A	A	A	C
	714	C	C	C	T	C

NOTE. Nucleotides at each position are given. In case these changes results in amino acid changes, they are indicated in parenthesis. *HA*, hemagglutinin gene; *NA*, neuraminidase gene; *NP*, nucleoprotein gene; *PA*, RNA polymerase gene.

[a] In each case, nucleotide numbering starts at the beginning of the open reading frame.

respiratory illness in the previous 8 months, and no new animals had entered the herd in the previous 9 months. Finally, molecular characterization studies showed that no molecular adaptive changes occurred and almost identical viruses infected humans and swine. There were only minor differences between human and swine pH1N1 isolates, which is likely, given the natural mutation rate of influenza virus both in vitro and in vivo [16, 17].

The duration of viral detection and clinical illness among swine is consistent with other Canadian reports [18]. The high rate (94%) of asymptomatic infections that we observed in swine may be attributed to the healthiness of the herd or some cross-protection rendered by previous vaccination. The A/Swine/Iowa/110600/00 H1N1 isolate in the vaccine offers some cross-protection against classical H1N1 viruses and reassortant H1N1 viruses [19].

In our study, one-third of humans with positive serological test results had few symptoms, and one-third were asymptomatic, so the ILI case definition was not sensitive for pH1N1 infection. Asymptomatic pH1N1 infections have been documented in studies from the United States [20], the United Kingdom [21], and France [22]. Our findings also correlate with results of seasonal influenza studies, in which 30%–50% of humans have few or no symptoms [23, 24, 25].

Although swine-to-human transmission of other strains of influenza has been reported [26, 27, 28, 29], there was no epidemiologic evidence of swine-to-human transmission of pH1N1 in this outbreak. There was also no evidence that passage of the pandemic virus in swine led to biologic changes in the virus. Our genomic sequencing studies showed that, 10 days after the virus was introduced into the herd, there was virtually no change in the virus at the molecular level.

This study has several limitations. First, only 2 humans had throat swab specimens that were positive for pH1N1 virus. The TAG RVP, used to screen throat swab specimens, has a sensitivity of 90.2% and a specificity of 100% for pH1N1, so it is possible that some positive samples were not detected [11]. Throat swab specimens, although acceptable, are not optimal to detect pH1N1 by RT-PCR [30]. We performed throat swabs to comply with a public health directive explicitly forbidding nasopharyngeal swabbing and aspirates in community settings [31]. Although the use of throat swab specimens for testing for the presence of virus may have contributed to the lack of positive RT-PCR results, it is more likely that humans with ILI were no longer shedding virus 2 weeks after their illness, when the swab specimens were taken [32]. Secondly, some individuals may have been incorrectly classified as positive for pH1N1 on the basis of cross-reactive serological test results. For example, ~5% of staff may have had cross-reactive antibodies to pH1N1 from previous swine flu infections, seasonal vaccination, or vaccination for swine flu in 1976 [33–35]. To minimize bias from cross reactive serological test results, we compared acute and convalescent phase serological test results, compared serological analysis of pH1N1 and seasonal influenza strains, and statistically ruled out correlation between positive pH1N1 serological test results and age or prior receipt of the seasonal influenza vaccine. Finally, there may have been recall bias when responding to the survey (eg, in remembering symptoms from the previous month). Although this would not affect our observation that humans were the source of this outbreak, it would affect the sensitivity and specificity calculations of the case definitions.

In summary, findings from this outbreak on a swine research farm in Alberta, Canada, support human-to-swine transmission. In both species, the virus caused mild illness without sequelae.

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Potential conflicts of interest. All authors: no conflicts.

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